

RESULT 2

ADF93964/c

ID ADF93964 standard; DNA; 50 BP.

XX

AC ADF93964;

XX

DT 11-MAR-2004 (first entry)

XX

DE Microorganism detection probe, SEQ ID 57.

XX

KW Probe; detection; identification; microorganism; food; drug;

KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.

XX

OS Staphylococcus epidermidis.

XX

PN WC2003106676-A1.

XX

PD 24-DEC-2003.

XX

PF 16-JUN-2003; 2003WO-JP007620.

XX

PR 14-JUN-2002; 2002JP-00174564.

XX

PA (HISF) HITACHI SOFTWARE ENG CO LTD.

PA (MITS) MITSUBISHI KAGAKU BIO-CHEMICAL LAB INC.

XX

PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;

PI Shimadzu M, Kobayashi I, Ishiko H;

XX

DR WPI; 2004-071565/07.

XX

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a

PT microorganism for specific detection and identification of the

PT microorganism in foods and drug compositions.

XX

PS Claim 2; SEQ ID NO 57; 150pp; Japanese.

XX

The present invention relates to probes (ADF93908-ADF94059) for the specific detection and identification of harmful microorganisms in samples of foods and drug compositions. The probe sequences are derived from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism or its complementary sequence. Detection and identification of the microorganism is by amplification of the complete 16S rRNA gene using primers ADF94060 and ADF94061, labelling the amplification product (a fluorescence label is preferred), and hybridising to the probe or probes of the invention. The probes may be immobilised on a DNA chip. The microorganism is selected from *Actinobacillus actinomycetemcomitans*, *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas maltophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Gitrobacter freundii*, *Veillonella parvula*, *Providencia stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*, *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*, *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium aquatium*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*

SEQ ID NO6 7 8.txt

CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
 CC gordonae.
 XX
 SQ Sequence 50 BP; 10 A; 12 C; 20 G; 8 T; 0 U; 0 Other;

Query Match 100.0% Score 15; DB 2; Length 50;
 Best Local Similarity 100.0%
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTCGTCTGTTGGC 15
 |||||
 Db 17 TCCTCGTCTGTTGGC 3

ESULT 3
 ADF93950/c

ID ADF93950 standard; DNA; 50 BP.
 XX
 AC ADF93950;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Microorganism detection probe, SEQ ID 43.
 XX
 KW Probe; detection; identification; microorganism; food; drug;
 KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
 XX
 OS Staphylococcus hominis.
 XX
 PN ~~WC~~2003106676-A1.
 XX
 PD 24-DEC-2003.
 XX
 PF 16-JUN-2003; 2003~~WO~~-JP007620.
 XX
 PR 14-JUN-2002; 2002JP-00174564.
 XX
 PA (HISF) HITACHI SOFTWARE ENG CO LTD.
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
 XX
 PI Hashida J, Ueno S, Mito I, Naruse K, Tamura M, Matsuda K;
 PI Shimadzu M, Kobayashi I, Ishiko H;
 XX
 DR WPI; 2004-071565/07.
 XX
 PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
 PT microorganism for specific detection and identification of the
 PT microorganism in foods and drug compositions.
 XX
 PS Claim 2; SEQ ID NO 43; 150pp; Japanese.
 XX
 CC The present invention relates to probes (ADF93908-ADF94059) for the
 CC specific detection and identification of harmful microorganisms in
 CC samples of foods and drug compositions. The probe sequences are derived
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism
 CC or its complementary sequence. Detection and identification of the
 CC microorganism is by amplification of the complete 16S rRNA gene using
 CC primers ADF94060 and ADF94061, labelling the amplification product (a
 CC fluorescence label is preferred), and hybridising to the probe or probes

SEQ ID NO: 7 8.txt

of the invention. The probes may be immobilised on a DNA chip. The microorganisms selected from *Actinobacillus actinomycetemcomitans*, *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas maltophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*, *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*, *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium aquatium*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus casseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*, *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium goodii*.

Sequence 50 BP; 10 A; 11 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 100.0% Score 15; DB 2; Length 50;
Best Local Similarity 100.0%
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTOGTCTGTTCG 15
| | | | | | | | | | | | | | |
Db 17 TCCTOGTCTGTTCG 3

SEQ ID NO: 6

SULT 2

ADF93953/c

ID ADF93953 standard; DNA; 50 BP.

XX

AC ADF93953;

XX

DT 11-MAR-2004 (first entry)

XX

DE Microorganism detection probe, SEQ ID 46.

XX

KW Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.

XX

OS *Staphylococcus warneri*.

XX

PN WO2003106676-A1.

XX

PD 24-DEC-2003.

XX

PF 16-JUN-2003; 2003WO-JP007620.

XX

PR 14-JUN-2002; 2002JP-00174564.

XX

PA (HISF) HITACHI SOFTWARE ENGINEERING LTD.

PA (M TS-) M TSUBI SHI KAGAKU BI O-CL I NI CAL LAB I NC.

XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
PI Shimadzu M, Kobayashi I, Ishiko H;

XX WPI; 2004-071565/07.

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
PT microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.

XX
PS Claim 2; SEQ ID NO 46; 150pp; Japanese.

XX
CC The present invention relates to probes (ADF93908-ADF94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADF94060 and ADF94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,
CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*
CC *maltophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*
CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*
CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*
CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*
CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*
CC *aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*,
CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,
CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*,
CC *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*,
CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*
CC *aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*
CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*
CC *casseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*
CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*
CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*
CC *corrodens*, *Streptococcus pyogenes*, *Braxella catarrhalis*, *Legionella*
CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,
CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*
CC *gordonae*.

XX
SQ Sequence 50 BP; 11 A; 10 C; 19 G; 10 T; 0 U; 0 Other;

Query Match 100.0% Score 16; DB 2; Length 50;
Best Local Similarity 100.0%
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTATCTGTTGGC 16
|||
Db 18 CTCCTTATCTGTTGGC 3

SEQ ID NO: 7

ESULT 3
ADF93956/c
ID ADF93956 standard; DNA; 50 BP.
XX
AC ADF93956;

11-MAR-2004 (first entry)

Microorganism detection probe, SEQ ID 49.

Probe; detection; identification; microorganism; food; drug;
16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.

Staphylococcus haemolyticus.

WO2003106676-A1.

24-DEC-2003.

16-JUN-2003; 2003WO-JP007620.

14-JUN-2002; 2002JP-00174564.

(HISF) HITACHI SOFTWARE ENG CO LTD.

(MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.

Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
Shimadzu M, Kobayashi I, Ishiko H;

WPI; 2004-071565/07.

20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
microorganism for specific detection and identification of the
microorganism in foods and drug compositions.

Claim 2; SEQ ID NO 49; 150pp; Japanese.

The present invention relates to probes (ADF93908-ADF94059) for the
specific detection and identification of harmful microorganisms in
samples of foods and drug compositions. The probe sequences are derived
from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism
or its complementary sequence. Detection and identification of the
microorganism is by amplification of the complete 16S rRNA gene using
primers ADF94060 and ADF94061, labelling the amplification product (a
fluorescence label is preferred), and hybridising to the probe or probes
of the invention. The probes may be immobilised on a DNA chip. The
microorganism is selected from *Actinobacillus actinomycetemcomitans*,
Acinetobacter calcoaceticus, *Haemophilus influenzae*, *Stenotrophomonas*
maltophilia, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*
aeruginosa, *Gltobacter freundii*, *Veillonella parvula*, *Providencia*
stuartii, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*
morganii, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*
warneri, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*
aerogenes, *Staphylococcus epidermidis*, *Streptococcus constellatus*,
Serratia marcescens, *Streptococcus anginosus*, *Escherichia coli*,
Klebsiella pneumoniae, *Enterococcus faecalis*, *Enterococcus faecium*,
Streptococcus sanguis, *Streptococcus mitis*, *Streptococcus intermedius*,
Listeria monocytogenes, *Clostridium perfringens*, *Corynebacterium*
aquaticum, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*
meningitidis, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*
casseliflavus, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*
typhi, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*
oxytoca, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*
corrodens, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*
pneumophila, *Mycobacterium tuberculosis*, *Mycobacterium avium*,
Mycobacterium intracellulare, *Mycobacterium kansasii* or *Mycobacterium*
gordonae.

SEQ ID NO: 6 7 8.txt
 SQ Sequence 50 BP; 11 A; 11 C; 19 G; 9 T; 0 U; 0 Other;
 Query Match 100.0% Score 16; DB 2; Length 50;
 Best Local Similarity 100.0%
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCTTGTCTGTTCGC 16
 |||||
 Db 18 CTCTTGTCTGTTCGC 3

SEQ ID NO: 8